



CC library. The probe for the screening was prepared by reverse  
 CC transcription on HepG2 mRNA followed by PCR using primers 09170-1  
 CC to produce a probe of 170-200 bp. The screening isolated the full  
 CC length sequence of the transcription factor. The gene was inserted into  
 CC expression vectors pBluescript KS and pCDV1 for expression of the  
 CC protein in COS7 cells, respectively. The ETS transcription  
 CC factor has specifically been activated by ras. It is useful as a  
 CC reagent in studies for the elucidation of the mechanism of cancer cell  
 CC multiplication or polyoma virus transformation of cells.  
 SQ Sequence 520 AA.

Query Match 4.2% Score 14; DB 1; Length 520;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANIDLSRS 308  
 DB 412 KNRPMANIDLSRS 425

RESULT 3  
 M00167  
 ID M00167 standard; Protein: 462 AA.  
 AC M00167;  
 DT 25-APR-1997 (first entry)  
 DE E1AF: matrix metalloproteinase regulator.  
 KM E1AF: matrix metalloproteinase; regulator; infiltration: cancer;  
 KM metastasis: cell; control; antisense: decoy; DNA binding region;  
 KM mammary cancer; fibrosarcoma; osteosarcoma; lung cancer.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT domain 315..399  
 FT /note= "DNA binding domain"  
 FT region 126..222  
 FT /note= "glutamine rich region"  
 PF M09624379-A1.  
 PF 15-AUG-1996;  
 PF 09-JAN-1996; J00016.  
 PR (8-FEB-1995; JP-020173.  
 PR (TAKI ) TAKARA SHUZO CO LTD.  
 PA Fujinaga K, Higashino F, Yoshida K;  
 DT Nucleic Acids Res 23:38422-38427/98.  
 DR Nucleic Acids Res 23:38422-38427/98.  
 PT Control of cancer cell infiltration by E1AF gene expression  
 PT regulation - also diagnosis of cancer by detection of E1AF gene  
 PS expression products.  
 PS Example 5; Pages 38-42; 65pp; Japanese.  
 CC The present sequence is the E1AF protein, which is a matrix  
 CC metalloproteinase regulator. The infiltration and metastasis of  
 CC cancer cells can be controlled by regulating the expression and  
 CC induction of the E1AF gene. This may be accomplished by  
 CC inducing antisense DNA or the E1AF gene. This may be accomplished by  
 CC expressing the DNA binding region of the E1AF protein, the target  
 CC DNA for the DNA binding region of the E1AF protein, a decoy gene  
 CC corresponding to the E1AF gene mRNA. Cancer can be diagnosed by  
 CC detecting E1AF gene expression products, e.g. E1AF protein or mRNA.  
 CC These methods may be used in the treatment and diagnosis of cancer.  
 CC 9. mammary cancer, fibrosarcoma, osteosarcoma, lung cancer, etc.  
 SQ Sequence 462 AA.

Query Match 4.2% Score 14; DB 1; Length 462;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 363 KNRPMANIDLSRS 308  
 DB 363 KNRPMANIDLSRS 376

RESULT 4

M49010  
 ID M49010 standard; Protein: 555 AA.  
 AC M49010;  
 DT 20-OCT-1998 (first entry)  
 DE Polyomavirus PEA3 protein.  
 KM Polyomavirus enhancer activator; PEA3; tumour; suppressor; inhibitor;  
 KM transformation; HRR-2; neu promoter; metastasis; cancer.  
 OS Polyomavirus.  
 PN M09830585-A2.  
 PN M09830585-A2.  
 PD 16-JUL-1998;  
 PD 12-JAN-1998; U00880.  
 PD 12-JAN-1997; U5760835.  
 PA (PEX) HUMV TEXAS SYSTEM.  
 PI Hung M, Xiong X, Weng W, et al.  
 DR WPI: 98-359661/74.  
 DR N-PSDB: V32688.

PT Method for repressing transformation of cells - by contacting cell  
 PT with polyoma-virus enhancer activator 3, useful for, e.g. treating  
 PT or preventing cancer, tumorigenesis and metastasis  
 PT (abstract: page 71-72; 83pp; English).  
 CC This document is used for repressing transformation of a cell  
 CC which involves contacting the cell with a polyoma-virus enhancer  
 CC growth of a tumour in a mammal comprising introducing to the mammal  
 CC PEA3-encoding nucleic acid where the expression of PEA3 in the mammal  
 CC results in a decrease in the growth rate of the tumour. PEA3 can regulate  
 CC repressor.  
 CC tumorigenic or metastatic cell, a cell. It can be used for the  
 CC prevention and treatment of such transformation-driven events as cancer,  
 CC Sequence 555 AA.

Query Match 4.2% Score 14; DB 1; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KNRPMANIDLSRS 308  
 DB 456 KNRPMANIDLSRS 469

RESULT 5  
 R44556  
 ID R44556 standard; Protein: 452 AA.  
 AC R44556;  
 DT 26-MAY-1994 (first entry)  
 DE Human Hm-Fli-1 gene product.  
 KM Human Hm-Fli-1 gene product; chimeric; chimeric; Ewing sarcoma;  
 KM EWS gene; malignant; neuroectodermal tumour; human chromosome 11;  
 KM primitive peripheral neuroectodermal tumour; human chromosome 11;  
 KW human chromosome 22; ss.  
 OS Homo sapiens.  
 PN M09323549-A.  
 PN M09323549-A.  
 PD 25-NOV-1993;  
 PD 20-MAY-1992; F00644.  
 PR (CNRS ) CNRS CMT WAT, KRCV SCI,  
 PI Aurias A, Delattre O, Desmarte C, Melot T, Peter M;  
 PI Pivongsest B, Thomas G, Zucman J;  
 DR WPI: 93-386580/48.  
 DR N-PSDB: G50644.  
 PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene  
 PT sequence involved in chromosomal translocation, also detected  
 PT of Ewing sarcoma and osteosarcoma.  
 PS disclosure: fig 7, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 18



QY 300 MWYDKLSR 307  
DB 359 MWYDKLSR 366

## RESULT 9

ID Y01520 standard: Protein: 451 AA.  
AC Y01520:  
DE 23-JUN-1999 (first entry)  
DE Chicken C-11 protein.  
DE Chicken C-11 protein; cell calcification inhibiting activity;  
KW calcification inhibiting agent; c-erb protein; arthritis deformans;  
KW osteofactor; spinal column ligament.  
OS Gallus sp.  
PN J11075871.A.  
PD 23-MAR-1999.  
PF 29-MAY-1998: 166076.  
PR 18-JUN-1997: US-050297.  
PR 18-JUN-1997: US-050297.  
PA (CHUS) CHUGA PHARM. CO. LTD.  
PA (UYFE) UNIV PENNSYLVANIA.  
DR MPI: 99-257708/22.  
DR N-PSDB: X26551.  
PT An active protein for inhibiting cell calcification - useful for  
PT measuring the calcification of a cell, for diagnosing arthritis  
PT deformans or ossification of spinal column ligament  
PS C-erb protein.  
CC The present seq. 11pp; Japanese. chicken C-11 protein which has cell  
CC calcification inhibiting activity. This protein also decreases  
CC a cell calcification inhibiting agent containing c-erb. (521).  
CC The proteins are used for measuring the calcification of a cell for  
CC diagnosing arthritis deformans or ossification of spinal column ligament.  
SQ Sequence 451 AA:

Query Match 2.4%: Score 8; DB 1:  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 300 MWYDKLSR 307  
DB 332 MWYDKLSR 339

## RESULT 10

ID P81328 standard: Protein: 295 AA.  
AC P81328:  
DE 22-OCT-1990 (first entry)  
DE Immunoreactive human B-lymphotropic virus  
KW MO8080914-A; human B-lymphotropic virus.  
PN 15-DEC-1988.  
PD 27-MAY-1988: U01807.  
PF 01-JUN-1987: US-056563.  
PR (BAVU) Baylor Univ College; (USSH) US Dept of Health and Human Services.  
PR Chang NT, Chang TW, Fung MS-C, Fung M-C, Gallo RC, Wong-Staal F;  
M.P.: 86-368628/51.  
DR 19810220/51.  
PT New immunoreactive protein of human B lymphotropic virus - and encoding  
PT DNA sequences, useful as immunogens and for detecting specific Abs in  
PS blood. Disclosure; P: English.  
CC This is used to detect antibodies against HBV in biological fluids (esp.  
CC for screening human serum or plasma).  
SQ Sequence 295 AA:

Query Match 2.1%: Score 7; DB 1:  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 130 VLKDIET 136  
DB 96 VLKDIET 102

## RESULT 11

ID R13016 standard: Protein: 153 AA.  
AC R13016:  
DE 26-SEP-1991 (first entry)  
DE deacetylcephalosporin C acetyltransferase N-terminal.  
KW DAC; deacetylcephalosporin C synthetase; DNACS;  
KW deacetylcephalosporin C synthetase; DNACS; cefg gene.  
OS Acromonium chrysogenum ATCC 14553.  
PN EP-437378-A.  
PD 17-JUL-1991.  
PF 11-JUN-1991: 300225.  
PR 11-JUN-1991: 300225.  
PR 20-APR-1990: GB-008272.  
PA (GLAX) GLAXO GROUP LTD.  
PI Malsman NJ, Ramsden M;  
DR MPI: 91-209975/29.  
DR N-PSDB: Q12599.  
PT Recombinant DNA encoding deacetylcephalosporin - for high yield  
PT prodn. of cephalosporin C in transformed hosts, with increased  
PT claim 3 page 18/22 of enzyme  
PS The cefg gene encoding the DNACS.  
CC A recombinant DNA construct encoding a gene encoding the  
CC DNACS/DACS. The construct enables efficient introduction of  
CC multiple and/or modified copies of a DAC acetyltransferase-encoding  
CC DNA sequence in hosts and hence the potential accumulation of  
CC a higher intracellular levels of cephalosporin C.  
SQ Sequence 153 AA:

Query Match 2.1%: Score 7; DB 1:  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 284 SAOYARL 290  
DB 4 SAOYARL 10

## RESULT 12

ID R42293 standard: Protein: 444 AA.  
AC R42293:  
DE 10-WAY-1994 (first entry)  
DE Cephalosporium acremonium  
KW acetylcephalosporin C acetyltransferase; cefg gene;  
KW Acromonium chrysogenum; antibiotic; biosynthesis; cefg; ss.  
PN EP-566897-A.  
PD 27-OCT-1993.  
PF 09-MAR-1993: 105016.  
PR (FAH) HOECHST AG 08966.  
PI Fernandez PJ, Gutierrez M, Martin MT, Velasco AJ,  
PI Fernandez Perrino FJ, Gutierrez Martin S, Martin Martin JF;  
PI Velasco Alvarez J;  
DR MPI: 93-337989/43.  
DR N-PSDB: Q50118.  
PT Cefg gene encoding DAC-ATP - used to enhance cephalosporin C  
PT claim 2; Page 6; 11pp; English.  
PS The cefg gene of C. acremonium encodes a protein of 444 amino acids  
CC having mol. wt. 49269 and having acetylcephalosporin C  
CC acetyltransferase activity. The isolated cefg gene encodes  
CC deacetylcephalosporin acetyltransferase deficiency and restores  
CC cephalosporin biosynthesis.

Sequence 444 AA:

Query Match 2.1%: Score 7, DB 1, Length 444:  
 Best Local Similarity 100.0%: Pred. No. 86:  
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

284 SNOVARL 290  
 |||||  
 4 SNOVARL 10

RESULT 13

667430 standard: Protein: 346 AA.  
 NC 667430: 1995 (first entry)  
 DE Thermostable aminopeptidase.  
 KW Aminopeptidase; thermostable; Pyrococcus furiosus; expression;  
 KM recombinant production.  
 OS Pyrococcus furiosus DMS3638.  
 PN J063195666-A.  
 PD 22-NOV-1994.  
 PR 18-MAY-1993: JP-138876.  
 RA TAKAI J, TAKANA SEIZO CO LTD.  
 DR N-25DB-075345-001.  
 PT Highly thermostable aminopeptidase gene - allows mass production  
 of aminopeptidase by culture of transformed organisms  
 PS Claim 2: Page 7-8: 10pp: Japanese.  
 CC Mass production of the aminopeptidase may be effected by  
 CC transforming a microbial host with a recombinant plasmid comprising  
 CC the aminopeptidase gene. The aminopeptidase is then expressed and  
 CC retrieved from the culture supernatant.  
 Sequence 346 AA:

Query Match 2.1%: Score 7, DB 1, Length 346:  
 Best Local Similarity 100.0%: Pred. No. 70:  
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

79 GASSREC 85  
 |||||  
 139 GASSREC 145

RESULT 14

W31186 standard: Protein: 905 AA.  
 AC W31186:  
 DT 11-MAR-1998 (first entry)  
 DE Human P22 polypeptide 1, 2.  
 KW Human P22 polypeptide 1; cell; B cell; development; activation;  
 KM modulation; cellular response; cell proliferation; autoimmune disease;  
 KM p55-Lck.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FI Domain 3..138  
 FI 11861-Leucine-21pep  
 FI Region 510..638  
 FI 650-672-poline/Lysine rich region\*  
 FI Region 650-672-poline/Lysine rich region\*  
 FT /note="glutamic acid rich region"  
 PD W09722285-A1.  
 PD 26-JUN-1997.  
 PR 11-DEC-1996: US-574959.  
 RA (DAND J) DNA FARMER CANCER INST. INC.  
 RA JOUNG J, SHIN J, Strominger JL, Vadmamdi RK:  
 RA N-PSDB: 789346.  
 DR CDNA encoding p57 and p160 and corresponding proteins - used in the

PT treatment of autoimmune disease and for T and B cell proliferation,  
 PT e.g. for treatment of tumours  
 PS Claim 84: Fig 11: 175pp: English.  
 CC This sequence represents a novel p160 polypeptide (160.2) which is  
 CC capable of activating transcription of a variety of genes upon activation  
 CC of p52 and is capable of binding to the p52/p56lck complex to modulate  
 CC the activity of the complex.  
 CC Response to p160 activation likely include those of which are involved in  
 CC T or B cell development/differentiation, T or B cell activation or  
 CC production of T or B cell specific factors e.g. lymphokines or  
 CC antibodies. This p160 polypeptide is also a substrate for  
 CC serine/threonine kinase activity. p160 polypeptides can modulate  
 CC degradation of cellular proteins e.g. cell cycle regulatory proteins  
 CC stimulating expression of cell cycle dependent kinase inhibitors and  
 CC arresting cell cycle progression at specific boundaries to thereby  
 CC modulate cell proliferation. As p160 boasts a cell response it may be  
 CC used in the treatment of autoimmune diseases.  
 CC pathogenic microorganisms p160 can be used to expand T cell populations  
 CC for treating infectious diseases or cancer and p160 inhibitors could  
 CC reduce B or T cell responses and may be used to treat a variety of  
 CC autoimmune diseases, e.g. diabetes mellitus, arthritis, multiple  
 CC sclerosis allergic reactions and Crohn's disease.  
 Sequence 905 AA:

Query Match 2.1%: Score 7, DB 1, Length 905:  
 Best Local Similarity 100.0%: Pred. No. 16e-02:  
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

13 PSHLLP 19  
 |||||  
 361 PSHLLP 367

RESULT 15

W35503 standard: Protein: 543 AA.  
 AC W35503:  
 DT 22-APR-1998 (first entry)  
 DE Human hyaluronate synthetase.  
 KW Hyaluronate synthetase; human; hyaluronic acid; drug preparation;  
 KM cosmetic preparation; gene therapy; carcinogenesis.  
 OS Homo sapiens.  
 FH Homo sapiens.  
 FI H07281138-A1.  
 PD 30-APR-1996: JP-109663.  
 PR 05-APR-1996: JP-084326.  
 RA (SEK ) SEIRAGANU CORP.  
 RA Itano N, Kimura K,  
 FI WP: 97-512726/47.  
 DR N-PSDB: 746713.  
 DE Human hyaluronate synthetase - for industrial scale  
 PT production of hyaluronic acid used in generating anti-carcinogenic  
 drugs or for cosmetics  
 PS Claim 2: Page 23-27: 35pp: Japanese.  
 CC This sequence represents a human hyaluronate synthetase, and is encoded  
 CC by the coding sequence of the invention. This enzyme is useful for  
 CC industrial scale production of hyaluronic acid for use in the preparation  
 CC of drugs and cosmetics. The drugs can also be used in compositions for  
 CC the treatment of disorders. The drugs can also be used for the preparation of antibodies  
 CC recognising hyaluronate synthetase, e.g. for diagnostic purposes.  
 CC Antisense DNA or RNA corresponding to the DNA can be used in gene therapy  
 CC treatment of carcinogenesis.  
 Sequence 543 AA:

Query Match 2.1%: Score 7, DB 1, Length 543:  
 Best Local Similarity 100.0%: Pred. No. 3e-02:  
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

31 AAGAVG 37

|||||||  
 Db 138 AAGAVG 144

Search completed: November 20, 1999, 15:35:23  
 Job time: 165 sec

GenCore version 4.5  
 Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 1999, 15:32:38 : Search time 13.1 seconds

(without alignments)  
 605.713 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 335

Sequence: 1 MGASAPGLSSVSPSHLLRP.....GIKKPDISRLVYFVHP 335

Scoring table: OLIGO

Searched: 188963 seqs, 23686106 residues

Database : A.Geneseq.36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of this alignment printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	4.2	155	1 R45451	Adipose tissue
2	14	4.2	520	1 R78185	ELAF-P
3	14	4.2	462	1 W00167	ELAF matrix metallo
4	14	4.2	555	1 W49010	Polyomavirus PPA3
5	14	4.2	452	1 W45556	Human HUN-FIL-1 ge
6	8	2.4	348	1 W07700	Human ETS2 repress
7	8	2.4	348	1 W07700	Mouse ETS2 repress
8	8	2.4	478	1 Y01521	Chicken c-erb prot
9	8	2.4	451	1 Y01520	Immunoreactive
10	7	2.1	295	1 R81328	Deacetylase
11	7	2.1	153	1 R13016	Cephalosporin ac
12	7	2.1	444	1 R42293	Thermostable amio
13	7	2.1	366	1 R67430	Human p160 polyep
14	7	2.1	366	1 W31186	Human hyaluronate
15	7	2.1	366	1 W31186	Human hyaluronan s
16	7	2.1	578	1 W26785	Human lymphoid-spe
17	7	2.1	531	1 W47237	Human secreted p20
18	7	2.1	581	1 W47238	Human secreted p20
19	7	2.1	359	1 W75169	Urinary tract BL21
20	7	2.1	89	1 W97655	Human 5' EST sece
21	7	2.1	93	1 W97657	Human 5' EST sece
22	7	2.1	14	1 P31133	Partial sequence o
23	6	1.8	14	1 P91468	Sequence of canina
24	6	1.8	284	1 P92071	Partial nucleotide
25	6	1.8	191	1 P92071	Sequence of canina
26	6	1.8	254	1 P93673	Sheep PRP gene for
27	6	1.8	256	1 P93674	Filamentous haemag
28	6	1.8	367	1 R03041	Sequence containin
29	6	1.8	367	1 R03041	Sequence containin
30	6	1.8	421	1 R05287	Immunogenic pneumo
31	6	1.8	471	1 R05287	Sequence of the
32	6	1.8	471	1 R05287	Part of canine sp
33	6	1.8	1664	1 R02024	Rat melanin-concen
34	6	1.8	1664	1 R02024	Adenyl cyclase fro
35	6	1.8	165	1 R07360	Heat resistant per
36	6	1.8	165	1 R08031	Sequence encoded b
37	6	1.8	165	1 R08031	Sequence encoded b
38	6	1.8	192	1 R02425	Sequence of the
39	6	1.8	927	1 P70768	Heat resistant per
40	6	1.8	5072	1 R11510	Sequence of part o
41	6	1.8	1445	1 R12108	Sequence of part o
42	6	1.8	1705	1 P94365	Sequence of part o
43	6	1.8	283	1 P81096	Sequence of filov

44 6 1.8 1522 1 P93357 Sequence of the ca  
45 6 1.8 528 1 W96151 Salmonella spp/LC

## ALIGNMENTS

## RESULT 1

ID R45451 standard: Protein: 155 AA.

AC R45451:  
DT 11-JUL-1994 (first entry)  
DE Adenovirus E1A-F protein.  
KW Adenovirus; cancer; ets oncogene; HeLa cell; enhancer core sequence;  
NM methylation.  
PN J05338975: Adenovirus.  
PD 14-DEC-1993.  
PF 02-JUN-1992: 165453.  
PR 02-JUN-1992: JP-165453.  
PA (TAKI ) TAKARA SHUZO CO LTD.  
DR WPI: 94-021923/03.  
NR N-PSDB: Q95149.  
RT Novel E1A-F gene - for production of adenovirus E1A-F and cancer  
PS Claim 1: Page 5: 7pp: Japanese.  
CC A clone comprising the adenovirus E1A-F gene was isolated by  
CC screening a HeLa cell cDNA library. The cDNA insert from the clone  
CC contains a 473bp open reading frame which codes for a protein  
CC having sequence R45451.  
SQ Sequence 155 AA:

Query Match 4.2%: Score 14; DB 1: length 155;  
Best Local Similarity 100.0%; Pval: No. 6 Re-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KRRPAMNYDKLSRS 308  
DB 56 KRRPAMNYDKLSRS 69

## RESULT 2

ID R78185 standard: Protein: 520 AA.

AC R78185:  
DT 09-FEB-1996 (first entry)  
DE Protein sequence of PEA3-beta -an ETS transcription factor.  
KW Transcription factor; probe; reverse transcription; PCR; primer;  
NM expression vector; E.coli; COS cell; ras; cancer cell multiplication;  
KM Polyoma virus; transformation.  
PN Homo sapiens.  
RT Location/Qualifiers  
FT misc\_difference 84  
FT misc\_difference 126  
FT misc\_difference 126  
FT misc\_difference 500  
FT /note= "encoded by CTC"  
FT /note= "encoded by AAC"  
FT /note= "encoded by ACC"  
PN J07145197-A.  
PD 06-JUN-1995.  
PF 23-NOV-1993: 29528393.  
PR 23-NOV-1993: JP-29528393.  
PA (ETSA ) ETSAT CO LTD.  
DR (HIRAW ) HIRANO T.  
DR WPI: 95-237197/31.  
NR N-PSDB: Q91769.  
RT ETS transcription factor activated by ras - may be used in the study  
RT of cancer cell proliferation and the proliferation of the polyoma  
RT virus  
PS Claim 1: Page 7-9: 9pp: Japanese.  
CC The amino acid sequence of the novel ETS transcription factor family  
CC member - PEA3-beta. The gene was isolated from a Hepo2 cell line cDNA

CC library. The probe for the screening was prepared by reverse  
CC transfection on Hep2 mRNA followed by PCR using primers Q91770-1,  
CC to produce a probe of 170-200 bp. The screening isolated the full  
CC length sequence of the transcription factor. The gene was inserted into  
CC the expression vectors pBluescript KS and pCDV1 for expression of the  
CC protein in E.coli and COS cells, respectively. The ETS transcription  
CC factor has specifically for and is activated by ras. It is useful as a  
CC reagent for the study of the role of the ETS family of cancer cell  
CC multiplication or polyoma virus transformation of cells.  
SQ Sequence 520 AA:

Query Match 4.2%: Score 14; DB 1: length 520;  
Best Local Similarity 100.0%; Pval: No. 1.9e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KRRPAMNYDKLSRS 308  
DB 412 KRRPAMNYDKLSRS 425

## RESULT 3

ID W00167 standard: Protein: 462 AA.

DT 25-JAN-1997 (first entry)  
DE E1A-F matrix metalloproteinase regulator.  
KW E1A-F matrix metalloproteinase; regulator; infiltration; cancer;  
KW metastasis; cell; control; antisense; decoy; DNA binding region;  
KW target DNA; ribosome; induction; diagnosis; detection; treatment;  
KW mammary cancer; fibrosarcoma; osteosarcoma; lung cancer.  
OS Homo sapiens.

FT key  
FT domain  
FT /note= "DNA binding domain"  
FT region  
FT /note= "glutamine rich region"

PN W09624379-A1.  
PD 15-AUG-1996.  
PF 09-JAN-1996: J00016.  
PR 08-FEB-1995: JP-020173.  
PA (TAKI ) TAKARA SHUZO CO LTD.  
DR Fujinaga K, Iizawa F, Yoshida K;  
DR N-PSDB: R37087/38.

PT Control of cancer cell infiltration by E1A-F gene expression  
PT regulation - also diagnosis of cancer by detection of E1A-F gene  
PT expression products  
PS Example 5: Pages 38-42: 65pp: Japanese.  
CC The present sequence is the E1A-F protein, which is a matrix  
CC metalloproteinase regulator. The infiltration and metastasis of  
CC cancer cells can be controlled by regulating the expression and  
CC regulation products of the E1A-F gene. This may be accomplished by  
CC expressing the DNA binding region of the E1A-F protein. The target  
CC DNA for the DNA binding region of the E1A-F protein or ribosomes  
CC corresponding to the E1A-F gene mRNA. Cancer can be diagnosed by  
CC detecting E1A-F gene expression products, e.g. E1A-F protein or mRNA.  
CC These methods may be used in the treatment and diagnosis of cancer,  
CC e.g. mammary cancer, fibrosarcoma, osteosarcoma, lung cancer, etc.  
SQ Sequence 462 AA:

Query Match 4.2%: Score 14; DB 1: length 462;  
Best Local Similarity 100.0%; Pval: No. 1.7e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 295 KRRPAMNYDKLSRS 308  
DB 363 KRRPAMNYDKLSRS 376

## RESULT 4





FT domain 21..98  
 FT /note= "DNA-binding domain  
 FT /note= "ets-like DNA binding domain"  
 FT domain 466..525  
 FT /label= Active-repressor-domain  
 FT W06939317-A1.  
 PD 12-DEC-1996.  
 PD 04-JUN-1996: U10177.  
 PR 05-JUN-1995: US-469412.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PI Athanasios MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ;  
 PI Sgouras D N.;  
 DR WPI: 97-043139/04.  
 DR N-PSDB: 147200.  
 PT New DNA encoding ETS2 repressor factor - useful for reducing  
 PS human gene expression associated with tumor cells  
 PS D102192-126 70372-1013P. Epub ahead of print.  
 CC Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS  
 CC family and acts as a transcriptional repressor in mammalian cells.  
 CC Its amino acid sequence was deduced from the murine ERF gene  
 CC (747198). Human ERF (see also W07700) has also been identified.  
 CC ERF has tumor suppressor activity. Chimeric molecules comprising  
 CC the ERF repressor domain in combination with a heterologous  
 CC transcription factor having a binding domain can be used to reduce  
 CC tumorigenicity associated with inappropriate expression of  
 CC the transcription factors.  
 CC Sequence 543 AA.

Query Match 2.4%: Score 8; DB 1; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 300 MWYDKLSR 307  
 Db 68 MWYDKLSR 75

RESULT 8  
 Y01521  
 ID Y01521 standard: Protein: 478 AA.  
 AC Y01521.  
 DE Chicken c-erg protein.  
 DE Chicken c-erg protein; cell calcification inhibiting activity;  
 KW cell calcification inhibiting agent; c-erg protein; arthritis deformans;  
 OS ossification; spinal column ligament.  
 OS Gallus sp.  
 PN J11075871-A.  
 PD 23-MAR-1999.  
 PD 23-MAR-1998: 166076.  
 PF 20-JUN-1997: US-050297.  
 PR 18-JUN-1997: US-878177.  
 PA (CHUS) CHUGAI PHARM CO LTD.  
 PA (UYPE) UNIV PENNSYLVANIA.  
 DR WPI: 99-257708/22.  
 DR N-PSDB: 826552.  
 PT An active protein for inhibiting cell calcification - useful for  
 PT measuring the calcification of a cell, for diagnosing arthritis  
 PT deformans or ossification of spinal column ligament  
 PS This sequence represents chicken C-erg protein. The specification  
 PS also describes a chicken C-11 protein (Y01520) which has cell  
 CC calcification inhibiting activity and a cell calcification inhibiting  
 CC agent containing c-erg protein. The proteins are used for measuring the  
 CC calcification of a cell, for diagnosing arthritis deformans or  
 CC ossification of spinal column ligament.  
 CC Sequence 478 AA.

Query Match 2.4%: Score 8; DB 1; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 300 MWYDKLSR 307  
 Db 359 MWYDKLSR 366

RESULT 9  
 Y01520  
 ID Y01520 standard: Protein: 451 AA.  
 AC Y01520.  
 DE 23-JUN-1999 (first entry)  
 DE Chicken C-11 protein.  
 KW Chicken C-11 protein; cell calcification inhibiting activity;  
 KW cell calcification inhibiting agent; c-erg protein; arthritis deformans;  
 OS ossification; spinal column ligament.  
 OS Gallus sp.  
 PN J11075871-A.  
 PD 23-MAR-1999.  
 PD 23-MAR-1998: 166076.  
 PF 20-JUN-1997: US-050297.  
 PR 18-JUN-1997: US-878177.  
 PA (CHUS) CHUGAI PHARM CO LTD.  
 PA (UYPE) UNIV PENNSYLVANIA.  
 DR WPI: 99-257708/22.  
 DR N-PSDB: 826552.  
 PT A protein for inhibiting cell calcification - useful for  
 PT measuring the calcification of a cell, for diagnosing arthritis  
 PT deformans or ossification of spinal column ligament  
 PS This sequence represents a chicken C-11 protein which has cell  
 CC calcification inhibiting activity. The specification also describes  
 CC a cell calcification inhibiting agent containing c-erg protein (Y01521).  
 CC The proteins are used for measuring the calcification of a cell, for  
 CC diagnosing arthritis deformans or ossification of spinal column ligament.  
 CC Sequence 451 AA.

Query Match 2.4%: Score 8; DB 1; Length 451;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 300 MWYDKLSR 307  
 Db 332 MWYDKLSR 339  
 RESULT 10  
 P81328  
 ID P81328 standard: Protein: 295 AA.  
 AC P81328.  
 DE 22-OCT-1990 (first entry)  
 DE Immunoreactive human B-lymphotropic viral protein  
 DE Immunoreactive: human B-lymphotropic virus.  
 PN M08080914-C.  
 PD 15-DEC-1988.  
 PF 27-MAY-1988: U01807.  
 PR 01-JUN-1987: US-056963.  
 PA (BAYV) Baylor Univ College; (USSH) US Dept of Health and Human Services.  
 PA Chang NT, Chang TM, Fung MS-C, Fung M-C, Gallo RC, Wong-Staal F;  
 DR WPI: 88-168828/51.  
 DR N-PSDB: 861128/51.  
 PT A nucleocapsid protein of human B lymphotropic virus - and encoding  
 PT DNA sequences, useful as immunogens and for detecting specific Abs in  
 PT blood  
 PS This is used: P: English.  
 PS This is used to detect antibodies against HBV in biological fluids (esp.  
 CC for screening human serum or plasma).  
 CC Sequence 295 AA.

Query Match 2.1%: Score 7; DB 1; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



PT treatment of autoimmune disease and for T and B cell proliferation.  
 PS e.g. for treatment of tumours  
 PS Claim 84: Fig 11: 175pp; English.  
 CC This sequence represents a novel p160 polypeptide (160.2) which is  
 CC capable of activating transcription of a variety of genes upon activation  
 CC of p52 and is capable of binding to the p52/p55lbp complex to modulate  
 CC Lck function in a manner similar to p52. The genes transcribed in  
 CC response to p160 activation likely include those of which are involved in  
 CC production of T or B cell specific factors e.g. lymphokines or  
 CC antibodies. This p160 polypeptide is also a substrate for  
 CC serine/threonine kinase activity. p160 polypeptides can modulate  
 CC degradation of cellular proteins e.g. cell cycle regulatory proteins  
 CC stimulating expression of cell cycle dependent kinase inhibitors and  
 CC arresting cell cycle progression at specific boundaries to thereby  
 CC modulate cell proliferation. As p160 boosts B cell response it may be  
 CC used to treat disorders where this is beneficial, e.g. infections by  
 CC immunosuppressive agents, immunodeficiency, and immunological disorders  
 CC for treating infectious diseases on cancer and p160 inhibitors could  
 CC reduce B or T cell responses and may be used to treat a variety of  
 CC autoimmune diseases, e.g. diabetes mellitus, arthritis, multiple  
 CC sclerosis allergic reactions and Crohn's disease.  
 SQ Sequence 905 AA;

Query Match 2.1% Score 7; DB 1; Length 905;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PSHLLP 19  
 |||||  
 DB 361 PSHLLP 367

RESULT 15  
 ID M36503 standard: Protein: 543 AA.  
 AC M36503;  
 DT 22-APR-1998 (first entry)  
 DE Human hyaluronate synthetase.  
 KW Hyaluronate synthetase; human; hyaluronic acid; drug preparation;  
 KW cosmetic preparation; gene therapy; carcinogenesis.  
 PS Homo sapiens.  
 PS M36503.12.1.  
 PD 16-OCT-1997.  
 PE 31-MAR-1997; J01111.  
 PR 30-APR-1996; JP-109663.  
 PR 05-APR-1996; JP-084326.  
 PA (SECK) SEIKAGAKU CORP.  
 PI Ikeno N, Kinoshita K;  
 WP: 97-512726/47.  
 DR M36503.12.1.  
 DR M36503.12.1.  
 PT production of hyaluronic acid used in generating anti-carcinogenic  
 PT drugs or for cosmetics  
 PS Claim 2: Page 23-27: 39pp; Japanese.  
 CC This sequence represents a human hyaluronate synthetase, and is encoded  
 CC by the coding sequence of the invention. This enzyme is useful for  
 CC industrial scale production of hyaluronic acid for use in the preparation  
 CC of drugs and cosmetics. The drugs can also be used in compositions for  
 CC the treatment of disorders involving the lowering of hyaluronic acid  
 CC production. The peptides may be used for the preparation of antibodies  
 CC to hyaluronate synthetase.  
 CC Antisense DNA or RNA corresponding to the DNA can be used in gene therapy  
 CC treatment of carcinogenesis.  
 SQ Sequence 543 AA;

DB 138 AAAGVG 144  
 |||||  
 Search completed: November 20, 1999, 15:35:23  
 Job time: 165 sec

Query Match 2.1% Score 7; DB 1; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 31 AAAGVG 37

**THIS PAGE BLANK (USPTO)**